



SEQUENCE LISTING

<110> DAI, KEN-SHW0

<120> HUMAN ARL-RELATED GENE VARIANTS ASSOCIATED WITH CANCER

<130> U014798-3

<140> 10/653,681

<141> 2003-09-02

<160> 4

<170> PatentIn version 3.2

<210> 1

<211> 1090

<212> DNA

<213> ARTIFICIAL SEQUENCE

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<223> VARIANT OF HUMAN ALDOSE REDUCTASE-LIKE GENE

<220>

<221> CDS

<222> (70)..(333)

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gcaccaacc atg gcc acg ttt gtg gag ctc agt acc aaa gcc aag atg ccc 111

Met Ala Thr Phe Val Glu Leu Ser Thr Lys Ala Lys Met Pro
1 5 10

att gtg ggc ctg ggc act tgg aag tct cct ctc ggc aaa gtg aaa gaa 159

Ile Val Gly Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu
15 20 25 30

gca gtg aag gtg gcc att gat gca gga tat cgg cac att gac tgt gcc 207

Ala Val Lys Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala
35 40 45

tat gtc tat cag aat gaa cat gaa gtg ggg gaa gcc atc caa gag aag 255

Tyr Val Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys
50 55 60

atc caa gag aag gct gtg aag cgg gag gac ctg ttc atc gtc agc aag 303

Ile Gln Glu Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys
65 70 75

ttg tgg ccc act tcc aga tcg aga agc tct tgaacaaacc tggactgaaa 353

Leu Trp Pro Thr Ser Arg Ser Arg Ser Ser
80 85

tataaaccag tgactaacca ggttgagtgt cacccatacc tcacgcagga gaaactgac 413

cagtactgcc actccaaggg catcaccgtt acggcctaca gccccctggg ctctccggat 473

agaccttggg ccaagccaga agacccttcc ctgctggagg atcccaagat taaggagatt 533

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gctgcaaagc acaaaaaaac cgcagcccag gttctgatcc gtttccatat ccagaggaat      593
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gactttaaat tgagtgatga ggagatggca accataactca gcttcaacag aaactggagg      713
gcctgtaacg tgttgcaatc ctctcatttg gaagactatc ccttcgatgc agaataattga      773
ggttgaatct cctggtgaga ttatacagga gattctcttt cttcgctgaa gtgtgactac      833
ctccactcat gtcccatttt agccaagctt atttaagatc acagtgaact tagtcctgtt      893
atagacgaga atcgagggtgc tgttttagac atttatttct gtatgttcaa ctaggatcag      953
aatatcacag aaaagcatgg cttgaataag gaaatgacaa tttttccac ttatctgatc     1013
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<220>
<223> PEPTIDE ENCODED BY VARIANT OF HUMAN ALDOSE REDUCTASE-LIKE GENE

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Gly Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu Ala Val
          20          25          30

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Lys Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala Tyr Val
          35          40          45

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Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys Ile Gln
          50          55          60

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Glu Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys Leu Trp
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Pro Thr Ser Arg Ser Arg Ser Ser
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<210> 3
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      Met Ala Thr Phe Val Glu Leu Ser Thr Lys Ala Lys Met Pro
      1              5              10

att gtg ggc ctg ggc act tgg aag tct cct ctc ggc aaa gtg aaa gaa      159
Ile Val Gly Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu
15              20              25              30

gca gtg aag gtg gcc att gat gca gga tat cgg cac att gac tgt gcc      207
Ala Val Lys Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala
      35              40              45

tat gtc tat cag aat gaa cat gaa gtg ggg gaa gcc atc caa gag aag      255
Tyr Val Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys
      50              55              60

atc caa gag aag gct gtg aag cgg gag gac ctg ttc atc gtc agc aag      303
Ile Gln Glu Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys
      65              70              75

ttg tgg ccc act ttc ttt gag aga ccc ctt gtg agg aaa gcc ttt gag      351
Leu Trp Pro Thr Phe Phe Glu Arg Pro Leu Val Arg Lys Ala Phe Glu
      80              85              90

aag acc ctc aag gac ctg aag ctg agc tat ctg gac gtc tat ctt att      399
Lys Thr Leu Lys Asp Leu Lys Leu Ser Tyr Leu Asp Val Tyr Leu Ile
      95              100              105              110

cac tgg cca cag gga ttc aag tct ggg gat gac ctt ttc ccc aaa gat      447
His Trp Pro Gln Gly Phe Lys Ser Gly Asp Asp Leu Phe Pro Lys Asp
      115              120              125

gat aaa ggt aat gcc atc ggt gga aaa gca acg ttc ttg gat gcc tgg      495
Asp Lys Gly Asn Ala Ile Gly Gly Lys Ala Thr Phe Leu Asp Ala Trp
      130              135              140

gag gcc atg gag gag ctg gtg gat gag ggg ctg gtg aaa gcc ctt ggg      543
Glu Ala Met Glu Glu Leu Val Asp Glu Gly Leu Val Lys Ala Leu Gly
      145              150              155

gtc tcc aat ttc agc cac ttc cag atc gag aag ctc ttg aac aaa cct      591
Val Ser Asn Phe Ser His Phe Gln Ile Glu Lys Leu Leu Asn Lys Pro
      160              165              170

gga ctg aaa tat aaa cca gtg act aac cag gtt gag tgt cac cca tac      639
Gly Leu Lys Tyr Lys Pro Val Thr Asn Gln Val Glu Cys His Pro Tyr
      175              180              185              190

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ctc acg cag gag aaa ctg atc cag tac tgc cac tcc aag ggc atc acc	687
Leu Thr Gln Glu Lys Leu Ile Gln Tyr Cys His Ser Lys Gly Ile Thr	
195 200 205	
gtt acg gcc tac agc ccc ctg ggc tct ccg gat aga cct tgg gcc aag	735
Val Thr Ala Tyr Ser Pro Leu Gly Ser Pro Asp Arg Pro Trp Ala Lys	
210 215 220	
cca gaa gac cct tcc ctg ctg gag gat ccc aag att aag gag att gct	783
Pro Glu Asp Pro Ser Leu Leu Glu Asp Pro Lys Ile Lys Glu Ile Ala	
225 230 235	
gca aag cac tcc cca agt ctg tgacaccagc acgcattggt gagaacattc	834
Ala Lys His Ser Pro Ser Leu	
240 245	
aggctctttga ctttaaattg agtgatgagg agatggcaac catactcagc ttcaacagaa	894
actggagggc ctgtaacgtg ttgcaatcct ctcatcttga agactatccc ttcgatgcag	954
aatattgagg ttgaatctcc tgggtgagatt atacaggaga ttctctttct tcgctgaagt	1014
gtgactacct ccactcatgt cccatttttag ccaagcttat ttaagatcac agtgaactta	1074
gtcctgttat agacgagaat cgagggtgctg ttttagacat ttatttctgt atgttcaact	1134
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<210> 4
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 <212> PRT
 <213> ARTIFICIAL SEQUENCE

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Met Ala Thr Phe Val Glu Leu Ser Thr Lys Ala Lys Met Pro Ile Val
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Gly Leu Gly Thr Trp Lys Ser Pro Leu Gly Lys Val Lys Glu Ala Val
20 25 30

Lys Val Ala Ile Asp Ala Gly Tyr Arg His Ile Asp Cys Ala Tyr Val
35 40 45

Tyr Gln Asn Glu His Glu Val Gly Glu Ala Ile Gln Glu Lys Ile Gln
50 55 60

Glu Lys Ala Val Lys Arg Glu Asp Leu Phe Ile Val Ser Lys Leu Trp

65	70					75					80				
Pro	Thr	Phe	Phe	Glu	Arg	Pro	Leu	Val	Arg	Lys	Ala	Phe	Glu	Lys	Thr
				85					90					95	
Leu	Lys	Asp	Leu	Lys	Leu	Ser	Tyr	Leu	Asp	Val	Tyr	Leu	Ile	His	Trp
			100					105					110		
Pro	Gln	Gly	Phe	Lys	Ser	Gly	Asp	Asp	Leu	Phe	Pro	Lys	Asp	Asp	Lys
		115					120					125			
Gly	Asn	Ala	Ile	Gly	Gly	Lys	Ala	Thr	Phe	Leu	Asp	Ala	Trp	Glu	Ala
	130					135					140				
Met	Glu	Glu	Leu	Val	Asp	Glu	Gly	Leu	Val	Lys	Ala	Leu	Gly	Val	Ser
145					150					155					160
Asn	Phe	Ser	His	Phe	Gln	Ile	Glu	Lys	Leu	Leu	Asn	Lys	Pro	Gly	Leu
				165					170					175	
Lys	Tyr	Lys	Pro	Val	Thr	Asn	Gln	Val	Glu	Cys	His	Pro	Tyr	Leu	Thr
			180					185					190		
Gln	Glu	Lys	Leu	Ile	Gln	Tyr	Cys	His	Ser	Lys	Gly	Ile	Thr	Val	Thr
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Ala	Tyr	Ser	Pro	Leu	Gly	Ser	Pro	Asp	Arg	Pro	Trp	Ala	Lys	Pro	Glu
	210					215					220				
Asp	Pro	Ser	Leu	Leu	Glu	Asp	Pro	Lys	Ile	Lys	Glu	Ile	Ala	Ala	Lys
225					230					235					240
His	Ser	Pro	Ser	Leu											
				245											